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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/030,537	04/23/2002	Balasulojini Karunanandaa	16516.130	4151

7590 12/07/2004

David R Marsh
Arnold & Porter
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Washington, DC 20004

EXAMINER	
KALLIS, RUSSELL	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 12/07/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/030,537	KARUNANANDAA ET AL.	
	Examiner	Art Unit	
	Russell Kallis	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-46* is/are pending in the application.

4a) Of the above claim(s) *1-15,22-24,28,29 and 42-46* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *16-21,25-27 and 30-41* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *3/28/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *additional sequence info*.

DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group I, Claims 1-21, 25-27 and 30-41 and further election of SEQ ID NO: 33 and SEQ ID NO: 4 in the reply filed on 9/07/04 is acknowledged. The traversal is on the ground(s) that there is no serious burden in examining all the claims together and that the Examiner has not shown that a search and examination of the entire application would cause a serious burden. This is not found persuasive because Applicant has not provided any evidence or arguments that the inventions of Groups I-VIII could be examined without a serious burden upon the office becausew the inventions of Groups I-VIII would each require separate consideration.

The requirement is still deemed proper and is therefore made FINAL.

Claims 1-46 are pending. Claims 1-15, 22-24, 28-29 and 42-46 are withdrawn as being drawn to non-elected Groups II-VIII or a non-elected sequence. Claims 16-21, 25-27 and 30-41 are examined.

Specification

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. (See page 13 lines 14-15 of the specification).

Claim Objections

Claims 37 and 40 are objected to because of the following informalities: At Claim 37, line 2, and at Claim 40, line 2, improper Markush terminology is employed, insert --consisting-- before "of" in line 2. See MPEP 2173.05(h). Appropriate correction is required.

Claims 25 and 36 are objected to because of the following informalities: The claims recite non-elected subject material of SEQ ID NO: 30, 31, 32 and 34. Applicant must remove non-elected material from the claims. Appropriate correction is required.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:
Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c).

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 21, 25-27 and 30-41 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant broadly claims a substantially purified nucleic acid molecule comprising a nucleic acid sequence encoding a plant HES1 protein; a plant comprising a nucleic acid sequence encoding a HES1 protein, a fragment of a HES1 protein, or a fragment of the amino acid sequence of SEQ ID NO: 33; and a method of producing a plant that expresses a HES1 protein.

Applicant describes plant nucleic acids of SEQ ID NO: 1-4 encoding amino acids of SEQ ID NO: 30-33, and nucleic acid sequence SEQ ID NO: 5 from yeast encoding a yeast HES1 protein of SEQ ID NO: 35.

Applicant does not describe any substantially purified nucleic acid molecules from a plant encoding a protein that has HES1 activity; any fragments of a exogenous structural nucleic acid of a multitude of lengths encoding a fragment of the amino acid sequence of SEQ ID NO: 33 or a fragment of a HES1 protein; or any substantially purified nucleic acid molecules comprising nucleic acid sequences encoding a HES1 protein other than SEQ ID NO: 5 encoding SEQ ID NO: 35 from yeast. Therefore, it is not clear that Applicant was in possession of the invention as broadly claimed.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. The court stated that, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of nucleic acid sequences from plants that encode a protein having HES1 activity, nucleic acid sequences encoding HES1 proteins, nucleic acid sequences encoding fragments of SEQ ID NO: 33 or fragments of a HES1 protein. Applicants only describe SEQ ID NO: 1-4 encoding SEQ ID NO: 30-33 of unspecified activity and nucleic acid sequence SEQ ID NO: 5 from yeast encoding a yeast HES1 protein of SEQ ID NO: 35, and thus Applicants fail to describe structural features common to members of the claimed genus of nucleic acid sequences encoding proteins having HES1 activity from plants or from other organisms, or fragments of HES1 proteins or fragments of SEQ ID NO: 33. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for HES1 activity, it remains unclear what features identify a HES1 protein or a HES1 protein from plants or from other organisms, or fragments of HES1 proteins, or fragments of SEQ ID NO: 33. Since the genus of nucleic acids encoding HES1 proteins from plants or from other species, or fragments thereof has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Claims 16-21, 25-27 and 30-41 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by

one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

Applicant broadly claims a substantially purified nucleic acid molecule comprising a nucleic acid sequence encoding a HES1 protein that hybridizes under conditions of high or low stringency to SEQ ID NO: 4 and encodes SEQ ID NO: 33; a substantially purified nucleic acid molecule comprising a nucleic acid sequence encoding a HES1 protein or a plant HES1 protein; a plant comprising a nucleic acid sequence encoding a HES1 protein, a fragment of a HES1 protein, or a fragment of the amino acid sequence of SEQ ID NO: 33; and a method of producing a plant that expresses a HES1 protein.

Applicant teaches the identification of putative HES1 coding sequences by blast homology based identification of putative orthologs to a yeast HES1 coding sequence using cDNA libraries from soybean, maize, and *Arabidopsis* and sequences available in public databases (Example 2 pages 61-62).

Applicant does not teach the other DNA nucleic acids encompassed by a substantially purified nucleic acid molecule that encodes a HES1 protein and the substantially purified nucleic acid molecule that encodes a plant HES1 protein, or nucleic acid sequences encoding fragments of HES1 proteins or SEQ ID NO: 33, and therefore since Applicant has not taught that the encoded putative HES1 proteins from plants or the broadly claimed HES1 of unspecified source have HES1 activity, then they have not taught how to make and/or use DNA encoding a HES1

protein, plants transformed therewith, or methods of producing plants that express a HES1 protein and that have increased levels of phyotsterols.

The state of the art for predicting protein function based upon sequence identities that vary within a relatively narrow range can be better understood when considering the methodology used to make such assertions and is made evident by experimental examples where a small number of changes introduced into proteins resulted in a change in the substrate preference of an enzyme and when structural relatedness cannot be translated into common function.

The state of the art for computer analysis of nucleic acid sequences is unpredictable because there are a number of inaccuracies that arise when attempting to make function predictions for DNA sequences that have no known function other than that based on homology of which several that have been documented by researchers in the field. To illustrate the difficulties, Doerks *et al.*, (TIG, 14: 248-250 1998 pg 248, right column, 2nd paragraph) produces a table of BLAST results from an uncharacterized protein family that includes quite a few proteins with annotations. They state "Only one can give a clue about functional features; others are simply wrong, misleading or uninformative". He continues, "There were even examples in which homologues scored best in PSI-BLAST that did not have the same catalytic activity". It is well established that sequence similarity is not sufficient to determine functionality of a DNA coding sequence. Doerks *et al.* state that computer analysis of genome sequences is flawed, and "overpredictions are common because the highest scoring database protein does not necessarily share the same or even similar functions" (the last sentence of the first paragraph of page 248). Doerks *et al.* also teach homologues that did not have the same catalytic activity because active

site residues were not conserved (page 248, the first sentence of the last paragraph). In addition, Smith *et al.* (Nature Biotechnology 15:1222-1223, November 1997) teach "there are numerous cases in which proteins of very different functions are homologous" (page 1222, the first sentence of the last paragraph). Also, Brenner (TIG 15, 4:132-133, April 1999) discusses the problem of inferring function from homology, stating "most homologs must have different molecular and cellular functions" (see the second full paragraph of the second column of page 132, for example). Furthermore, Bork *et al.* (TIG 12, 10:425-427, October 1996) teach numerous problems with the sequence databases that can result in the misinterpretation of sequence data. Bork *et al.* discussing the same topic state " search methods are stretched and spurious hits are taken as real. Moreover, similarities might only be restricted to certain domains, but the function is transferred to a whole protein" (pg 426, right column, 1st paragraph). Moreover, Venter C. *et al.*, Science, 2001; Vol. 291, pp. 1304-1351 state on page 1334 last column to page 1335 column 3, that prediction of gene function with respect to assignment of function using predictive algorithms produces results replete with false positives.

The state of the art for isolation of a homologous sequence encoding the a protein having the same activity using only homology to predict function is inherently unpredictable, and is illustrated in an example where a small number of changes to the coding region for a strict desaturase resulted in an enzyme with a hydroxylase activity demonstrating that a small number of changes to the coding region of a desaturase could account for the functional divergence seen across a range of enzymes involved in fatty acid metabolism (Broun *et al.* Science Vol. 282 13 November 1998; Abstract lines 4-6 and p. 1317 column 1, lines 51-56). The problem of assigning function from structure is further exacerbated by the fact that the prior art does not

support a clear function for the structure of the nucleic acids of the claims. Fang M. *et al.* The EMBO Journal; Vol. 15, No. 23; pages 6447-6459 teaches on page 6449 column 1 beginning with the new section to the end of the section in column 2; that there is a lack of functional relatedness among yeast OSBP homologs that includes HES1, and that HES1 mutants in yeast alone or in combination with other OSBP mutations did not restore growth as did the KES1 homolog, suggesting that HES1 alone would not produce a detectable phenotype in a transformed plant. In addition, a sequence comparison between the amino acid sequence of HES1 from yeast and SEQ ID NO: 33 shows significant gaps and that the two proteins are of a different size suggesting that isolated nucleic acid sequence SEQ ID NO: 4 encoding SEQ ID NO: 33 would require further undue trial and error experimentation to determine its' activity. Moreover, it is also important to note that Applicant has not performed the most routine of scientific procedures known in the art, namely functional complementation of a mutant in yeast or some other organism to show how to make and/or use the claimed invention.

Given the lack of guidance in the instant specification, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through a multitude of homologous nucleic acids and fragments thereof and test for HES1 activity, either *in vivo* or *in planta*.

Therefore, given the breadth of the claims; the lack of guidance and working examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

All claims are rejected.

Claims 16-21, 25-27 and 31-40 are deemed free of the prior art given the failure of the prior art to teach or reasonably suggest a nucleic acid sequence encoding a plant HES1 protein, plants transformed with a nucleic acid sequence encoding a HES1 protein and a method of expressing a HES1 protein in a plant.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Kallis whose telephone number is (571) 272-0798. The examiner can normally be reached on M-F 8:30-5.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (571) 272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Russell Kallis

Russell Kallis Ph.D.
November 28, 2004

Db 412 EDLSSIHWRF 421

RESULT 4
KES1_YEAST
ID KES1_YEAST STANDARD; PRT; 434 AA.
AC P35844;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE KES1 protein (Oxysterol-binding protein homolog 4).
GN Name=KES1; Synonyms=OSH4; OrderedLocusNames=YPL145C;
GN ORFNames=LPI3C, P2614;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94287711; PubMed=8017104;
RA Jiang B., Brown J.L., Sheraton J., Fortin N., Bussey H.;
RT "A new family of yeast genes implicated in ergosterol synthesis is
RT related to the human oxysterol binding protein.";
RL Yeast 10:341-353(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97103777; PubMed=8948103;
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of 55 kb on the left arm of yeast chromosome XVI
RT identifies a small nuclear RNA, a new putative protein kinase and two
RT new putative regulators.";
RL Yeast 12:1483-1492(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [4]
RP GENETIC ANALYSIS.
RX MEDLINE=21135676; PubMed=11238399;
RA Beh C.T., Cool L., Phillips J., Rine J.;
RT "Overlapping functions of the yeast oxysterol-binding protein
RT homologues.";
RL Genetics 157:1117-1140(2001).
CC -!- FUNCTION: Plays a role in ergosterol synthesis.
CC -!- SIMILARITY: Belongs to the OSBP family.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---

DR EMBL; U03913; AAA17736.1; -.
DR EMBL; U43703; AAB68217.1; -.
DR EMBL; X96770; CAA65548.1; -.
DR EMBL; Z73501; CAA97849.1; -.
DR PIR; S42676; S42676.
DR GermOnline; 144127; -.
DR SGD; S0006066; KES1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0006694; P:steroid biosynthesis; IGI.
DR GO; GO:0016192; P:vesicle-mediated transport; IGI.
DR InterPro; IPR000648; Oxysterol_BP.
DR Pfam; PF01237; Oxysterol_BP; 1.
DR PROSITE; PS01013; OSBP; 1.
KW Sterol biosynthesis.
SQ SEQUENCE 434 AA; 49492 MW; 360E4A46ABE2D87B CRC64;

Query Match 44.2%; Score 957.5; DB 1; Length 434;
Best Local Similarity 49.1%; Pred. No. 1.5e-61;
Matches 211; Conservative 56; Mismatches 100; Indels 63; Gaps 12;

```
Qy          13 ASKTSWSSFLKSIASFNGDLSSLTAPPFILSTTSLTEYSAYWCEHPALFVAPA------- 65
               || :||:|||||||||||||||||:|||||||  ||||:| || ||| ||: |:
Db           5 ASSSSWTSFLKSIASFNGDLSSLSAPPFILSPISLTEFSQYWAEHPELFLEPSFINDDNY 64

Qy          66 ----------REPDPAKRALLVLKWFLSTLHQQYCSRSEKLGSEKKPLNPFLGELFLGKW 115
                         |: | | | | |||:|||  |||||:| ||||||||||||||||:|||
Db          65 KEHCLIDPEVESPELA-RMLAVTKWFISTLKSQYCSRNESLGSEKKPLNPFLGELFVGKW 123

Qy         116 IEDE--DVGETRLISEQVSHHPPATAYSIVNEKHGVELQGYNAQKASFSSTIQ--VKQLG 171
                 |  : ||| |:|||||||| ||:|| |:|: |:||||  ||||: ::   ||| |
Db         124 ENKEHPEFGETVLLSEQVSHHPPVTAFSIFNDKNKVKLQGYNQIKASFTKSLMLTVKQFG 183

Qy         172 HAYLSLTPPGKDANNEDDREHYLITLPNLHIESLIYGTPFVELEKSCKIASSTGYISKID 231
               |  | :    ||        | ||:| | |||| ::  :||||||    | |||| :  |:
Db         184 HTMLDI----KD--------ESYLVTPPPLHIEGILVASPFVELEGKSYIQSSTGLLCVIE 232

Qy         232 FSGKGWLSGKKNTFSAVLYKESDGEKN---PLYTADGQWSSSFTIRDARAKKDIETF-TI 287
               |||:|: |||||:| | :||:|   |:    |||  |||| |  |  |  |::   |
Db         233 FSGRGYFSGKKNSFKARIYKDSKDSKDKEKALYTISGQWSGSSKIIKANKKEESRLFYDA 292

Qy         288 SNLKTTPLTVAPLDEQDEWETRRAWRDVAAAIERGDMEATSNAKTKIEVAQRELRKKEKE 347
               : :   | | ||:||   |:|:|| ||| ||: ||    :  ||:|  ||||||:|:
Db         293 ARIPAEHLNVKPLEEQHPLESRKAWYDVAGAIKLGDFNLIAKTKTELEETQRELRKEEEA 352

Qy         348 QGEEWERRFFK----------RVNEKDEPTFMRLAAMLDLTQ---------GIESDRT 386
               :|  |:||:||           | |||: ||::||: |:|:          | : ||
Db         353 KGISWQRRWFKDFDYSVTPEEGALVPEKDD-TFLKLASALNLSTKNAPSGTLVGDKEDRK 411

Qy         387 GGV----WRF 392
                 :    |||
Db         412 EDLSSIHWRF 421
```

RESULT 5
Q6CRP3
ID Q6CRP3 PRELIMINARY; PRT; 415 AA.
AC Q6CRP3;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Strain NRRL Y-1140 chromosome D of strain NRRL Y-1140 of Kluyveromyces
DE lactis.
GN ORFNames=KLLA0D07480g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,